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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/912,252

DATE: 12/31/2002

TIME: 14:08:19

Input Set : A:\Berlx-79.app

Output Set: N:\CRF4\12312002\I912252.raw

3 <110> APPLICANT: Croze, Ed  
 4 Vogel, David  
 5 Russell-Harde, Dean  
 7 <120> TITLE OF INVENTION: THE USE OF AN INTERFERON RECEPTOR POLYPEPTIDE  
 8 CHAIN TO ENHANCE THE EFFECTS OF INTERFERONS  
 10 <130> FILE REFERENCE: Berlx 79  
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/912,252  
 C--> 13 <141> CURRENT FILING DATE: 2000-06-26  
 15 <160> NUMBER OF SEQ ID NOS: 4  
 17 <170> SOFTWARE: PatentIn Ver. 2.1  
 19 <210> SEQ ID NO: 1  
 20 <211> LENGTH: 513  
 21 <212> TYPE: PRT  
 22 <213> ORGANISM: Murine sp.  
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 29 20 25 30  
 31 Gly Tyr Pro Asp Glu Pro Cys Thr Ile Asn Ile Thr Ile Arg Asn Ser  
 32 35 40 45  
 34 Arg Leu Ile Leu Ser Trp Glu Leu Glu Asn Lys Ser Gly Pro Pro Ala  
 35 50 55 60  
 37 Asn Tyr Thr Leu Trp Tyr Thr Val Met Ser Lys Asp Glu Asn Leu Thr  
 38 65 70 75 80  
 40 Lys Val Lys Asn Cys Ser Asp Thr Thr Lys Ser Ser Cys Asp Val Thr  
 41 85 90 95  
 43 Asp Lys Trp Leu Glu Gly Met Glu Ser Tyr Val Val Ala Ile Val Ile  
 44 100 105 110  
 46 Val His Arg Gly Asp Leu Thr Val Cys Arg Cys Ser Asp Tyr Ile Val  
 47 115 120 125  
 49 Pro Ala Asn Ala Pro Leu Glu Pro Pro Glu Phe Glu Ile Val Gly Phe  
 50 130 135 140  
 52 Thr Asp His Ile Asn Val Thr Met Glu Phe Pro Pro Val Thr Ser Lys  
 53 145 150 155 160  
 55 Ile Ile Gln Glu Lys Met Lys Thr Thr Pro Phe Val Ile Lys Glu Gln  
 56 165 170 175  
 58 Ile Gly Asp Ser Val Arg Lys Lys His Glu Pro Lys Val Asn Asn Val  
 59 180 185 190  
 61 Thr Gly Asn Phe Thr Phe Val Leu Arg Asp Leu Leu Pro Lys Thr Asn  
 62 195 200 205  
 64 Tyr Cys Val Ser Leu Tyr Phe Asp Asp Asp Pro Ala Ile Lys Ser Pro  
 65 210 215 220

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67 Leu Lys Cys Ile Val Leu Gln Pro Gly Gln Glu Ser Gly Leu Ser Glu
68 225                230                235                240
70 Ser Ala Ile Val Gly Ile Thr Thr Ser Cys Leu Val Val Met Val Phe
71                245                250                255
73 Val Ser Thr Ile Val Met Leu Lys Arg Ile Gly Tyr Ile Cys Leu Lys
74                260                265                270
76 Asp Asn Leu Pro Asn Val Leu Asn Phe Arg His Phe Leu Thr Trp Ile
77                275                280                285
79 Ile Pro Glu Arg Ser Pro Ser Glu Ala Ile Asp Arg Leu Glu Ile Ile
80                290                295                300
82 Pro Thr Asn Lys Lys Lys Arg Leu Trp Asn Tyr Asp Tyr Glu Asp Gly
83 305                310                315                320
85 Ser Asp Ser Asp Glu Glu Val Pro Thr Ala Ser Val Thr Gly Tyr Thr
86                325                330                335
88 Met His Glu Leu Thr Gly Lys Pro Leu Gln Gln Thr Ser Asp Thr Ser
89                340                345                350
91 Ala Ser Pro Glu Asp Pro Leu His Glu Glu Asp Ser Gly Ala Glu Glu
92                355                360                365
94 Ser Asp Glu Ala Gly Ala Gly Ala Gly Ala Glu Pro Glu Leu Pro Thr
95                370                375                380
97 Glu Ala Gly Ala Gly Pro Ser Glu Asp Pro Thr Gly Pro Tyr Glu Arg
98 385                390                395                400
100 Arg Lys Ser Val Leu Glu Asp Ser Phe Pro Arg Glu Asp Asn Ser Ser
101                405                410                415
103 Met Asp Glu Pro Gly Asp Asn Ile Ile Phe Asn Val Ser Leu Asn Ser
104                420                425                430
106 Val Phe Leu Arg Val Leu His Asp Glu Asp Ala Ser Glu Thr Leu Ser
107                435                440                445
109 Leu Glu Glu Asp Thr Ile Leu Leu Asp Glu Gly Pro Gln Arg Thr Glu
110                450                455                460
112 Ser Asp Leu Arg Ile Ala Gly Gly Asp Arg Thr Gln Pro Pro Leu Pro
113 465                470                475                480
115 Ser Leu Pro Ser Gln Asp Leu Trp Thr Glu Asp Gly Ser Ser Glu Lys
116                485                490                495
118 Ser Asp Thr Ser Asp Ser Asp Ala Asp Val Gly Asp Gly Tyr Ile Met
119                500                505                510
121 Arg

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125 &lt;210&gt; SEQ ID NO: 2

126 &lt;211&gt; LENGTH: 2468

127 &lt;212&gt; TYPE: DNA

128 &lt;213&gt; ORGANISM: Murine sp.

130 &lt;400&gt; SEQUENCE: 2

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132 ggcgattcag gtgtgagagc agaaaaacgg acttaagagc tgagcaggat gcgttcacgg 120
133 tgcaccgtct ctgccgtcgg tctcctcagc ttgtgtcttg tgggtgtctgc gagcctagag 180
134 actatcacac cgtctgcttt tgatgggtat ccagatgaac cttgcactat aaacataaca 240
135 atacgaaatt cccggctaatt ttatccttgg gaattagaga acaagtcttg cccacccgct 300
136 aactacaccc tctggtacac agtcatgagc aaagacgaaa atctgacgaa ggtaagaac 360
137 tgttcagata ccacgaagtc atcatgtgac gtgacagata agtggttga gggcatggag 420

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138 agctacgtcg tgcgccatcgt catagtgcac agagggggact tgaccgtgtg ccgctgctca 480
139 gactacatcg tgccctgcaaa cgctcctctt gagccgccag aatttgagat cgttggcttt 540
140 acagaccaca taaacgtgac gatggaattt ccacctgtca cttccaaaat aatccaggaa 600
141 aagatgaaga ctacaccctt tgtcatcaaa gaacagatag gggacagcgt taggaagaag 660
142 cacgagccca aagtgaataa tgtcactggg aacttcacat ttgtccttag agacttactt 720
143 ccaaagacaa actactgtgt atctctttat tttgatgatg accccgcaat aaaatctccc 780
144 ttaaaatgca tcgtccttca gcctggccag gaatcaggat tatcagaatc tgctatagta 840
145 ggaataacta cttcgtgttt ggtagtgtat gttttcgtga gcactatcgt aatgctgaaa 900
146 cggattgggt atatatgcct aaaagacaat ttgcccaatg tcttgaactt ccgccacttt 960
147 ttaacctgga taatccctga acggtcacct tcagaagcca tcgatcggct ggaaatcatc 1020
148 cccacaaaaca agaagaagag actgtggaat tacgattatg aggatggcag tgacagtgc 1080
149 gaagaggtcc ccacagcaag tgtcactggc tacaccatgc atgaactgac gggcaagcct 1140
150 ctgcaacaaa cctctgacac ctccagccagc cccgaggatc ccctgcatga agaagattca 1200
151 ggcgctgagg aatctgatga agctggagca ggggctggag ctgagccaga actccccaca 1260
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153 ctcgaggact cattccccag ggaggacaac agctccatgg atgagcctgg ggacaacatt 1380
154 atcttcaacg tgagcttaaa ctctgtgttt ctgagggttc tccatgatga agatgcctca 1440
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162 ctttccacta atgcactaag gtggtttgtg ttacatttcc cagggaacag gttcagtgtg 1920
163 ttttcagagg cagcccaagg tctcctatcc ctatgttggt tcctaggaaa tgattaaatt 1980
164 ggggggagag aaagggaaaag aaaaactgcc caagcagtgt tcaggaggac tccagggaatg 2040
165 aacctgaaaag ggggcggaag ggtcagaggt aaggcatgct gagctggctg ctggcacaag 2100
166 aaaagccatc aaggtttgag cccctgctgt ctggggccct cccagatgtc aacatctgtc 2160
167 tcctctactc taggaagttc attcaccat aaagccccgc acagtgcacg tgaggagggg 2220
168 gagaagccgc aggaataatt ctaggatcca acgcgtgact cagagagagg gatatcatgg 2280
169 ccataattta aggtcatttc tcgtcaactc tttaaccttc agttttctca acttatgaaa 2340
170 taaagggact gagcaggtag gcttggggag agatgcccaa agtggatgaa ggggtgaggg 2400
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172 aaggactg 2468

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175 &lt;210&gt; SEQ ID NO: 3

176 &lt;211&gt; LENGTH: 515

177 &lt;212&gt; TYPE: PRT

178 &lt;213&gt; ORGANISM: Homo sapiens

180 &lt;400&gt; SEQUENCE: 3

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181 Met Leu Leu Ser Gln Asn Ala Phe Ile Phe Arg Ser Leu Asn Leu Val
182   1           5           10           15
184 Leu Met Val Tyr Ile Ser Leu Val Phe Gly Ile Ser Tyr Asp Ser Pro
185           20           25           30
187 Asp Tyr Thr Asp Glu Ser Cys Thr Phe Lys Ile Ser Leu Arg Asn Phe
188           35           40           45
190 Arg Ser Ile Leu Ser Trp Glu Leu Lys Asn His Ser Ile Val Pro Thr
191           50           55           60
193 His Tyr Thr Leu Leu Tyr Thr Ile Met Ser Lys Pro Glu Asp Leu Lys

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194 65          70          75          80
196 Val Val Lys Asn Cys Ala Asn Thr Thr Arg Ser Phe Cys Asp Leu Thr
197          85          90          95
199 Asp Glu Trp Arg Ser Thr His Glu Ala Tyr Val Thr Val Leu Glu Gly
200          100          105          110
202 Phe Ser Gly Asn Thr Thr Leu Phe Ser Cys Ser His Asn Phe Trp Leu
203          115          120          125
205 Ala Ile Asp Met Ser Phe Glu Pro Pro Glu Phe Glu Ile Val Gly Phe
206          130          135          140
208 Thr Asn His Ile Asn Val Val Val Lys Phe Pro Ser Ile Val Glu Glu
209 145          150          155          160
211 Glu Leu Gln Phe Asp Leu Ser Leu Val Ile Glu Glu Gln Ser Glu Gly
212          165          170          175
214 Ile Val Lys Lys His Lys Pro Glu Ile Lys Gly Asn Met Ser Gly Asn
215          180          185          190
217 Phe Thr Tyr Ile Ile Asp Lys Leu Ile Pro Asn Thr Asn Tyr Cys Val
218          195          200          205
220 Ser Val Tyr Leu Glu His Ser Asp Glu Gln Ala Val Ile Lys Ser Pro
221          210          215          220
223 Leu Lys Cys Thr Leu Leu Pro Pro Gly Gln Glu Ser Glu Ser Ala Glu
224 225          230          235          240
226 Ser Ala Lys Ile Gly Gly Ile Ile Thr Val Phe Leu Ile Ala Leu Val
227          245          250          255
229 Leu Thr Ser Thr Ile Val Thr Leu Lys Trp Ile Gly Tyr Ile Cys Leu
230          260          265          270
232 Arg Asn Ser Leu Pro Lys Val Leu Asn Phe His Asn Phe Leu Ala Trp
233          275          280          285
235 Pro Phe Pro Asn Leu Pro Pro Leu Glu Ala Met Asp Met Val Glu Val
236          290          295          300
238 Ile Tyr Ile Asn Arg Lys Lys Lys Val Trp Asp Tyr Asn Tyr Asp Asp
239 305          310          315          320
241 Glu Ser Asp Ser Asp Thr Glu Ala Ala Pro Arg Thr Ser Gly Gly Gly
242          325          330          335
244 Tyr Thr Met His Gly Leu Thr Val Arg Pro Leu Gly Gln Ala Ser Ala
245          340          345          350
247 Thr Ser Thr Glu Ser Gln Leu Ile Asp Pro Glu Ser Glu Glu Glu Pro
248          355          360          365
250 Asp Leu Pro Glu Val Asp Val Glu Leu Pro Thr Met Pro Lys Asp Ser
251          370          375          380
253 Pro Gln Gln Leu Glu Leu Ser Gly Pro Cys Glu Arg Arg Lys Ser
254 385          390          395          400
256 Pro Leu Gln Asp Pro Phe Pro Glu Glu Asp Tyr Ser Ser Thr Glu Gly
257          405          410          415
259 Ser Gly Gly Arg Ile Thr Phe Asn Val Asp Leu Asn Ser Val Phe Leu
260          420          425          430
262 Arg Val Leu Asp Asp Glu Asp Ser Asp Asp Leu Glu Ala Pro Leu Met
263          435          440          445
265 Leu Ser Ser His Leu Glu Glu Met Val Asp Pro Glu Asp Pro Asp Asn
266          450          455          460

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268 Val Gln Ser Asn His Leu Leu Ala Ser Gly Glu Gly Thr Gln Pro Thr
269 465                               470                               475                               480
271 Phe Pro Ser Pro Ser Ser Glu Gly Leu Trp Ser Glu Asp Ala Pro Ser
272                               485                               490                               495
274 Asp Gln Ser Asp Thr Ser Glu Ser Asp Val Asp Leu Gly Asp Gly Tyr
275                               500                               505                               510
277 Ile Met Arg
278                               515
281 <210> SEQ ID NO: 4
282 <211> LENGTH: 2636
283 <212> TYPE: DNA
284 <213> ORGANISM: Homo sapiens
286 <400> SEQUENCE: 4
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289 gtgtatatca gcctcgtggt ttggtatttc tatgattcgc ctgattacac agatgaatct 180
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322 tagctgggat tacaggcgcc tgccaccatg cctagcaaat ttttgtattt ttagtagaga 2160

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L:12 M:270 C: Current Application Number differs, Replaced Application Number

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date